



**RESULT 2**  
 US-10-664-456-13  
 ; Sequence 13, Application US/10664456  
 ; Publication No. US20040038364A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Immunex Corporation  
 ; TITLE OF INVENTION: NEW METALLOPROTEINASE-DISINTEGRIN FAMILY MEMBERS: SVPH  
 ; TITLE OF INVENTION: DNAs AND POLYPEPTIDES  
 ; FILE REFERENCE: 03260.0093-00304  
 ; CURRENT APPLICATION NUMBER: US/10/664,456  
 ; CURRENT FILING DATE: 2003-09-19  
 ; PRIOR APPLICATION NUMBER: prior APPLICATION NUMBER: US/09/890,323  
 ; PRIOR FILING DATE: prior FILING DATE: 2001-07-25  
 ; PRIOR APPLICATION NUMBER: 60/116,670  
 ; PRIOR FILING DATE: 1999-01-21  
 ; PRIOR APPLICATION NUMBER: 60/138,682  
 ; PRIOR FILING DATE: 1999-06-14  
 ; PRIOR APPLICATION NUMBER: 60/155,798  
 ; PRIOR FILING DATE: 1999-09-27  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 13  
 ; LENGTH: 787  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-664-456-13

Query Match 100.0%; Score 615; DB 12; Length 787;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-49;  
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 VHTKDIENVKRCGNGVVEEGECDGPLKHCACKDPCCLSNCNCTLTDGSTCAFGLCCDKCKF 60  
 Db 389 VHTKDIENVKRCGNGVVEEGECDGPLKHCACKDPCCLSNCNCTLTDGSTCAFGLCCDKCKF 448

Query 61 LPSGKVCRKEVNECDLPEWCNGTSHKCPDDFYVEDGIPCKERG 103  
 Db 449 LPSGKVCRKEVNECDLPEWCNGTSHKCPDDFYVEDGIPCKERG 491

**RESULT 3**  
 US-10-664-456-14  
 ; Sequence 14, Application US/10664456  
 ; Publication No. US20040038364A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Immunex Corporation  
 ; TITLE OF INVENTION: NEW METALLOPROTEINASE-DISINTEGRIN FAMILY MEMBERS: SVPH  
 ; TITLE OF INVENTION: DNAs AND POLYPEPTIDES  
 ; FILE REFERENCE: 03260.0093-00304  
 ; CURRENT APPLICATION NUMBER: US/10/664,456  
 ; CURRENT FILING DATE: 2003-09-19  
 ; PRIOR APPLICATION NUMBER: prior APPLICATION NUMBER: US/09/890,323  
 ; PRIOR FILING DATE: prior FILING DATE: 2001-07-25  
 ; PRIOR APPLICATION NUMBER: 60/116,670  
 ; PRIOR FILING DATE: 1999-01-21  
 ; PRIOR APPLICATION NUMBER: 60/138,682  
 ; PRIOR FILING DATE: 1999-06-14  
 ; PRIOR APPLICATION NUMBER: 60/155,798  
 ; PRIOR FILING DATE: 1999-09-27  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 14  
 ; LENGTH: 820  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-664-456-14

Query Match 100.0%; Score 615; DB 12; Length 820;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-49;  
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**RESULT 4**  
 US-10-408-765A-1252  
 ; Sequence 1252, Application US/10408765A  
 ; Publication No. US20040101874A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; APPLICANT: Fahy, Eoin D.  
 ; APPLICANT: Zhang, Bing  
 ; APPLICANT: Gibson, Bradford W.  
 ; APPLICANT: Taylor, Steven W.  
 ; APPLICANT: Glenn, Gary M.  
 ; APPLICANT: Warnock, Dale E.  
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
 ; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
 ; FILE REFERENCE: 660088.465  
 ; CURRENT APPLICATION NUMBER: US/10/408,765A  
 ; CURRENT FILING DATE: 2003-04-04  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 1252  
 ; LENGTH: 820  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-408-765A-1252

Query Match 100.0%; Score 615; DB 16; Length 820;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-49;  
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 VHTKDIENVKRCGNGVVEEGECDGPLKHCACKDPCCLSNCNCTLTDGSTCAFGLCCDKCKF 60  
 Db 389 VHTKDIENVKRCGNGVVEEGECDGPLKHCACKDPCCLSNCNCTLTDGSTCAFGLCCDKCKF 448

Query 61 LPSGKVCRKEVNECDLPEWCNGTSHKCPDDFYVEDGIPCKERG 103  
 Db 449 LPSGKVCRKEVNECDLPEWCNGTSHKCPDDFYVEDGIPCKERG 491

**RESULT 5**  
 US-09-792-200B-22  
 ; Sequence 22, Application US/09792200B  
 ; Patent No. US20020042368A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Immunex Corporation  
 ; APPLICANT: Fanslow, William C.  
 ; APPLICANT: Poindexter, Kurt  
 ; APPLICANT: Cerretti, Douglas P.  
 ; APPLICANT: Black, Roy A.  
 ; TITLE OF INVENTION: INTEGRIN ANTAGONISTS  
 ; FILE REFERENCE: 2958-A  
 ; CURRENT APPLICATION NUMBER: US/09/792,200B  
 ; CURRENT FILING DATE: 2001-02-23  
 ; PRIOR APPLICATION NUMBER: US 60/184,865  
 ; PRIOR FILING DATE: 2000-02-25  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 22  
 ; LENGTH: 528  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Fusion Construct  
 US-09-792-200B-22

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

סימן

Searched		Query	Match	Length	DB	ID	Description
1	615	100.0	766	3	AAB07739	Aab07739	A snake v
2	615	100.0	787	3	AAB07740	Aab07740	A snake v
3	615	100.0	820	3	AAB07741	Aab07741	A snake v
4	557	90.6	528	4	AAE13061	Aae13061	ADAM-29di
5	446	72.5	726	2	AY17413	Aay17413	Human SVP
6	446	72.5	726	2	AY03223	Aay03223	Amino aci
7	446	72.5	726	7	ADC78877	Adc78877	Human PRO
8	446	72.5	776	6	ABR39425	Abt39425	Human GEN
9	443	72.0	542	2	AY03224	Aay03224	Amino aci
10	443	72.0	722	2	AY28655	Aay28655	Human SVP
11	443	72.0	722	6	ABG76200	Abg76200	Human sna
12	431	70.1	535	2	AY17414	Aay17414	SVPH1-26
13	431	70.1	535	4	AAE13056	Aae13056	ADAM-20di
14	422	68.6	523	4	AAE13057	Aae13057	ADAM-21di
15	357	58.0	499	3	AAB07738	Aab07738	A snake v
16	357	58.0	781	3	AAB07743	Aab07743	A snake v
17	357	58.0	790	3	AAB07742	Aab07742	A snake v
18	357	58.0	790	3	AAB07705	Aab07705	Amino aci
19	357	58.0	790	4	AAU12273	Aau12273	Human PRO
20	357	58.0	790	6	ABO17717	Abo17717	Novel hum
21	357	58.0	790	6	ABU80971	Abu80971	Human PRO
22	357	58.0	790	6	ABU66671	Abu66671	Human PRO
23	357	58.0	790	6	ABU59752	Abu59752	Novel sec
24	357	58.0	790	6	ABO24942	Abo24942	Human sec

XX 21-JAN-2000; 2000WO-US001338.  
XX PR 21-JAN-1999; 99US-0116670P.  
XX PR 14-JUN-1999; 99US-0138682P.  
XX PR 27-SEP-1999; 99US-0155798P.  
XX PA (IMMV ) IMMUNEX CORP.  
XX PI Cerretti DP;  
XX DR 2000-4822914/42.  
XX DR N-PSDB; AAA59304.  
XX PT Snake venom protease (SVPH) nucleic acids, and polypeptides, used to  
PT identify proteins having metalloproteinase-disintegrin activity, and  
PT inhibitors of the proteins for use in therapeutics.  
XX PS Claim 13; Page 15; 105pp; English.  
XX CC The present sequence represents an alternatively spliced snake venom  
CC protease-1 (SVPH-1) polypeptide, designated SVPH-1a. The SVPH  
CC polypeptides are metalloproteinase-disintegrin protein family members.  
CC The SVPH polynucleotides can be used as probes to identify nucleic acids  
CC encoding proteins having metalloproteinase-disintegrin activity, to  
CC identify human chromosome 1 or 4, to map genes on those chromosomes, to  
CC identify genes associated with diseases, syndromes and conditions  
CC associated with the chromosomes, and to study proteinases and their  
CC activities on cell/cell interactions and the immune system. Sense or  
CC

CC of SVPH 1, 3, or 4. The SVPH polypeptides can be used to study cell/cell  
 CC and cell/matrix interactions involved in cellular processes and in the  
 CC immune system. The polypeptides may also be used to screen for inhibitors  
 CC of the polypeptide's activity, which are used in therapeutics. The  
 CC antibodies can be used in assays to detect the presence of the  
 CC polypeptides in vitro or in vivo, and to purify the polypeptides by  
 CC affinity chromatography  
 XX

SQ Sequence 766 AA;  
 Query Match 100.0%; Score 615; DB 3; Length 766;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-43;  
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VHTKDIIFNVKRCGNNGVVEEGECDCGPLXKHCAKDPCCLSNTLTDGSTCARGLCCDKCF 60  
 Db 389 VHTKDIIFNVKRCGNNGVVEEGECDCGPLXKHCAKDPCCLSNTLTDGSTCARGLCCDKCF 448  
 Qy 61 LPSGKVKCRKEVNECDLPEWCNGTSHKCPDDFYVEDGIPCKERG 103  
 Db 449 LPSGKVKCRKEVNECDLPEWCNGTSHKCPDDFYVEDGIPCKERG 491

## RESULT 2

AAB07740

ID AAB07740 standard; protein; 787 AA.

XX AC AAB07740;

XX DT 07-NOV-2000 (first entry)

XX DE A snake venom protease (SVPH-1) polypeptide variant SVPH-1b.

XX KW Snake venom protease; SVPH; SVPH-1; metalloproteinase-disintegrin;

XX KW chromosome 1; chromosome 4; immune system; splice variant.

XX OS Homo sapiens.

XX PN WO200043525-A2.

XX PD 27-JUL-2000.

XX PF 21-JAN-2000; 2000WO-US001338.

XX PR 21-JAN-1999; 99US-0116670P.

XX PR 14-JUN-1999; 99US-0138682P.

XX PR 27-SEP-1999; 99US-0155798P.

XX PA (IMMV ) IMMUNEX CORP.

XX PI Cerretti DP;

XX XX WPI; 2000-482914/42.

XX DR DR N-PSDB; AAA59306.

XX PS Claim 13; Page 15-16; 105pp; English.

XX XX The present sequence represents an alternatively spliced snake venom

CC protease-1 (SVPH-1) polypeptide, designated SVPH-1b. The SVPH

CC polypeptides are metalloproteinase-disintegrin protein family members.

CC The SVPH polynucleotides can be used as probes to identify nucleic acids

CC encoding proteins having metalloproteinase-disintegrin activity, to

CC identify human chromosome 1 or 4, to map genes on those chromosomes, to

CC identify genes associated with diseases, syndromes and conditions

CC associated with the chromosomes, and to study proteinases and their

CC activities on cell/cell interactions and the immune system. Sense or

CC antisense oligonucleotides of SVPH can be used to study cell/cell

CC and cell/matrix interactions involved in cellular processes and in the

CC immune system. The polypeptides may also be used to screen for inhibitors

CC of the polypeptide's activity, which are used in therapeutics. The

CC and cell/matrix interactions involved in cellular processes and in the

CC immune system. The polypeptides may also be used to screen for inhibitors  
 CC of the polypeptide's activity, which are used in therapeutics. The  
 CC antibodies can be used in assays to detect the presence of the  
 CC polypeptides in vitro or in vivo, and to purify the polypeptides by  
 CC affinity chromatography  
 XX

SQ Sequence 787 AA;

Query Match 100.0%; Score 615; DB 3; Length 787;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-43;  
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHTKDIIFNVKRCGNNGVVEEGECDCGPLXKHCAKDPCCLSNTLTDGSTCARGLCCDKCF 60

Db 389 VHTKDIIFNVKRCGNNGVVEEGECDCGPLXKHCAKDPCCLSNTLTDGSTCARGLCCDKCF 448

Qy 61 LPSGKVKCRKEVNECDLPEWCNGTSHKCPDDFYVEDGIPCKERG 103

Db 449 LPSGKVKCRKEVNECDLPEWCNGTSHKCPDDFYVEDGIPCKERG 491

## RESULT 3

AAB07741

ID AAB07741 standard; protein; 820 AA.

XX AC AAB07741;

XX DT 07-NOV-2000 (first entry)

XX DE A snake venom protease (SVPH-1) polypeptide variant SVPH-1c.

XX KW Snake venom protease; SVPH; SVPH-1; metalloproteinase-disintegrin;

XX KW chromosome 1; chromosome 4; immune system; splice variant.

XX OS Homo sapiens.

XX PN WO200043525-A2.

XX PD 27-JUL-2000.

XX PF 21-JAN-2000; 2000WO-US001338.

XX PR 21-JAN-1999; 99US-0116670P.

XX PR 14-JUN-1999; 99US-0138682P.

XX PR 27-SEP-1999; 99US-0155798P.

XX PA (IMMV ) IMMUNEX CORP.

XX PI Cerretti DP;

XX XX WPI; 2000-482914/42.

XX DR DR N-PSDB; AAA59306.

XX PS Claim 13; Page 16; 105pp; English.

CC The present sequence represents an alternatively spliced snake venom

CC protease-1 (SVPH-1) polypeptide, designated SVPH-1c. The SVPH

CC polypeptides are metalloproteinase-disintegrin protein family members.

CC The SVPH polynucleotides can be used as probes to identify nucleic acids

CC encoding proteins having metalloproteinase-disintegrin activity, to

CC identify human chromosome 1 or 4, to map genes on those chromosomes, to

CC identify genes associated with diseases, syndromes and conditions

CC associated with the chromosomes, and to study proteinases and their

CC activities on cell/cell interactions and the immune system. Sense or

CC antisense oligonucleotides of SVPH can be used to study cell/cell

CC and cell/matrix interactions involved in cellular processes and in the

CC immune system. The polypeptides may also be used to screen for inhibitors

CC of the polypeptide's activity, which are used in therapeutics. The

CC and cell/matrix interactions involved in cellular processes and in the

Copyright (c) 1993 - 2004 Compugen Ltd.  
 GenCore version 5.1.6  
 atrolysin A (EC 3.  
 metalloproteinase  
 ADAM 5 protein pre  
 platelet aggregati  
 ecarin precursor -  
 hemorrhagic protein  
 tMDC 1 protein - C  
 cyritestin precurs  
 hypothetical prote  
 platelet aggregati  
 bitan alpha - Puff  
 bitistatin - puff  
 trigramin precurso  
 applaggin - easter  
 platelet-aggregati  
 vascular apoptosis  
 30 240.5 39.1 610 2 JC7530  
 31 240 39.0 419 2 S41607  
 32 232 37.7 549 2 S48169  
 33 230.5 37.5 777 2 I48100  
 34 229 37.2 216 2 JX0265  
 35 229 37.2 616 2 A55796  
 36 227 36.9 416 2 A37877  
 37 218.5 35.5 736 2 S47645  
 38 218.5 35.5 823 2 S18968  
 39 215.5 35.0 1042 2 T26644  
 40 212 34.5 209 2 JX0266  
 41 191.5 31.1 83 2 F35982  
 42 183.5 29.8 83 2 A34156  
 615 US-10-664-456-12\_COPY\_389\_491  
 1 VHTKDIIFNVKRCGNNGVVEEG..... SHKCPPDDFYVEDGIPCKKRG 103  
 title:  
 perfect score:  
 sequence:  
 scoring table:  
 BLOSUM62

## APPENDIX 3: ALIGNMENTS

וְבָרָא יְהוָה כָּל־הָרָקֶב וְבָרָא יְהוָה כָּל־הָרֶבֶת.

minimum DB seq length: 0

הנִזְמָן לְמִשְׁמָרָה בְּבֵית הַמִּשְׁמָרָה

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Fahage : BIB 78:\*

1: piri:\*

2: *Pir2*;  
3: *Pir3*†

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

๘๘๘

Result No.	Score	Query Match	Length	DB	ID	Description
1	314	51.1	473	2	149283	ADAM 4 protein pre
2	306.5	49.8	655	2	JC7850	disintegrin and me
3	306.5	49.8	660	2	S71949	metalloproteinase
4	305.5	49.7	732	2	152361	testicular metallo
5	294	47.8	903	2	S60257	meltrin alpha - mo
6	293	47.6	713	2	I65253	disintegrin-like t
7	289.	47.0	735	2	I48101	ADAM 6 protein pre
8	282	45.9	825	2	S55060	fertilin alpha-II
9	282	45.9	905	2	S55059	fertilin alpha-I -
10	266	43.3	600	2	I49281	fertilin alpha pre
11	263.5	42.8	734	2	JC4861	fertilin beta cha
12	262	42.6	617	2	S48160	metalloproteinase
13	261	42.4	357	2	S23403	sperm surface prot
14	261	42.4	524	2	S38539	disintegrin-like m
15	261	42.4	670	2	I65967	disintegrin-like m
16	260.5	42.4	735	2	G02937	fertilin beta - cr
17	259	42.1	150	2	S60258	meltrin beta - mou
18	257	41.8	776	2	S28258	androgen-regulated
19	256	41.6	826	2	A60385	monocyte surface a
20	253	41.1	789	2	S28259	androgen-regulated
21	251.5	40.9	429	2	A42972	coagulation factor
22	251	40.8	571	2	S24789	jararhagin C precu
23	251	40.8	609	2	S55270	catrocollastatin p
24	250.5	40.7	512	2	T37819	probable zinc meta
25	249.5	40.6	952	2	T18900	disintegrin and me
26	249	40.5	419	2	A594414	metalloproteinase
27	245.5	39.9	814	2	G02390	disintegrin-like m
28	244.5	39.8	756	2	S47656	tMDC II protein -

RESULT 1  
 I49283  
 ADAM 4 PR  
 C;Species  
 C;Date: 0  
 C;Accession  
 R;Wolfsbe  
 Dev. Biol  
 A;Title:  
 A;Referen  
 A;Accessi  
 A;Status:  
 A;Molecul  
 A;Residue  
 A;Cross-r  
 C;Genetic  
 A;Gène:  
 C;Superfa  
 F;129-211  
 2000000  
 ear number or hits satisfying chosen parameters.  
 Minimum DB seq length: 0  
 Maximum DB seq length: 200000000  
 st-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries  
 Database : PIR\_78: \*  
 1: pir1: \*  
 2: pir2: \*  
 3: pir3: \*  
 4: pir4: \*  
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.  
 SUMMARIES

Query Match 49.8%; Score 306.5; DB 2; Length 655;  
 Best Local Similarity 49.5%; Pred. No. 9.4e-19;  
 Matches 48; Conservative 19; Mismatches 29; Indels 1; Gaps 1;

Qy 5 DIFNVKRCGNGVVEEGEECDCGPLKHCAKDPCCL-SNCTLTDGSTCAFGLCKDKCKFLPS 63  
 Db 410 EAYSAPPSCGNKLVDAGEECDCGTPKECELDPCCEGSTCKLKSFAECAYGDCCKDKCRFLPG 469

Qy 64 GKVRKEVNECDLPEWCGNTSHKCPDDFYVEDGIPCK 100  
 Db 470 GTLCRGKTCSECDVPEYCNGSQQFCQPDVFHQNGYPCQ 506

RESULT 3  
 S71949 metalloproteinase 12 (EC 3.4.24.-) precursor - human  
 metalloproteinase 12; myeloma cell metalloproteinase MCMP  
 N;Alternate names: disintegrin 12; myeloma  
 C;Species: Homo sapiens (man)  
 C;Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 04-Feb-2000  
 C;Accession: S71949; PC4264  
 R;McKie, N.; Dallas, D.J.; Edwards, T.; Apperley, J.F.; Russell, R.G.G.; Croucher, P.I.  
 Biochem. J. 318, 459-462, 1996  
 A;Title: Cloning of a novel membrane-linked metalloproteinase from human myeloma cells.  
 A;Reference number: S71949; PMID:8809033  
 A;Accession: S71949  
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-660 <McK>  
 A;Experimental source: myeloma cells<sup>B</sup>  
 R;McKie, N.; Edwards, T.; Dallas, D.J.; Houghton, A.; Stringer, B.; Graham, R.; Russell, J.  
 Biochem. Biophys. Res. Commun. 230, 335-339, 1997  
 A;Title: Expression of members of a novel membrane linked metalloproteinase family (ADAM)  
 A;Reference number: PC4263; MUID:9016778  
 A;Accession: PC4264  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-337 <McF>  
 A;Experimental source: articular chondrocyte  
 C;Function:  
 A;Description: involved in cell/cell and cell/matrix interaction in a variety of cell types  
 A;Note: membrane-bound; belongs to reprelysin family of metalloproteinases  
 C;Superfamily: mouse meltrin alpha; disintegrin homology  
 C;Keywords: hydrolase; metalloproteinase; zinc  
 F;1-24/Domain: signal sequence #status predicted <SIG>  
 F;25-660/Product: pre-metalloproteinase 12 #status predicted <MAT>  
 F;54-59/Region: autoinhibitory  
 F;295-378/Domain: disintegrin homology <DIS>  
 F;574-598/Region: epidermal growth factor-like  
 F;622-642/Domain: transmembrane #status predicted <TM1>  
 F;57-229-233,239/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted  
 F;229-233,239/Binding site: zinc, catalytic (His) (active) #status predicted  
 F;230/Active site: Glu #status predicted

Query Match 49.8%; Score 306.5; DB 2; Length 660;  
 Best Local Similarity 49.5%; Pred. No. 9.4e-19;  
 Matches 48; Conservative 19; Mismatches 29; Indels 1; Gaps 1;

Qy 5 DIFNVKRCGNGVVEEGEECDCGPLKHCAKDPCCL-SNCTLTDGSTCAFGLCKDKCKFLPS 63  
 Db 292 EAYSAPPSCGNKLVDAGEECDCGTPKECELDPCCEGSTCKLKSFAECAYGDCCKDKCRFLPG 351

Qy 64 GKVRKEVNECDLPEWCGNTSHKCPDDFYVEDGIPCK 100  
 Db 352 GTLCRGKTCSECDVPEYCNGSQQFCQPDVFHQNGYPCQ 388

RESULT 4  
 152361 testicular metalloproteinase-like, disintegrin-like, cysteine-rich protein IVa - crab-eating macaque  
 C;Species: Macaca fascicularis (crab-eating macaque)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jul-2000  
 C;Accession: 152361  
 A;Status: preliminary; translated from GB/EMBL/DBJ

RESULT 5  
 S60257 meltrin alpha - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 20-Jun-2000  
 C;Accession: S60257  
 R;Yagami-Hiroasa, T.; Sato, T.; Kuriyaki, T.; Kamijo, K.; Nabeshima, Y.I.; Fujisawa-Sehama, N.; Nature 377, 652-656, 1995  
 A;Title: A metalloprotease-disintegrin participating in myoblast fusion.  
 A;Reference number: S60257; MUID:96026308; PMID:7566181  
 A;Accession: S60257  
 A;Status: preliminary; nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-903 <YAG>  
 A;Cross-references: EMBL:D50411; NID:91054586; PID:BA008912.1; PMID:91054587  
 C;Superfamily: mouse meltrin alpha; disintegrin homology  
 F;421-503/Domain: disintegrin homology <DIS>  
 F;349/Active site: Glu #status predicted

Query Match 47.8%; Score 294; DB 2; Length 903;  
 Best Local Similarity 49.5%; Pred. No. 1.3e-17;  
 Matches 48; Conservative 12; Mismatches 37; Indels 0; Gaps 0;

Qy 4 KDIFNVKRCGNGVVEEGEECDCGPLKHCAKDPCCL-SNCTLTDGSTCAFGLCKDKCKFLPS 63  
 Db 417 KQAFGGRKRCGNGVVEEGEECDCGPEEECTNRCNNATTCLRPDAVCAHGGQCCEDCQLKPP 476

Query Match 64 GKVRKEVNECDLPEWCGNTSHKCPDDFYVEDGIPCK 100  
 Best Local Similarity 64.5%; Pred. No. 1.3e-17;  
 Matches 48; Conservative 12; Mismatches 37; Indels 0; Gaps 0;

Qy 64 GKVRKEVNECDLPEWCGNTSHKCPDDFYVEDGIPCK 100  
 Db 477 GTACRGSSNSCDLPEFCTGTAAPHCPANVYLHDGHPHQ 513

RESULT 6  
 165253 disintegrin-like testicular metalloproteinase (EC 3.4.24.-) IVb - crab-eating macaque (F-  
 C;Species: Macaca fascicularis (crab-eating macaque)  
 C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000  
 C;Accession: 165253  
 R;Perry, A.C.F.; Jones, R.; Hall, L.  
 Biochem. J. 312, 239-244, 1995  
 A;Title: Analysis of transcripts encoding novel members of the mammalian metalloprotease  
 C;Species: Macaca fascicularis (crab-eating macaque)  
 C;Accession: 165253  
 A;Status: preliminary; translated from GB/EMBL/DBJ



DR EMBL; AAF22163.1; - .

DR HSSP; P18619; 1FVL.

DR MEROPS; M12.981; - .

DR Genew; HGNC:207; ADAM29.

DR MIM; 604778; - .

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0008237; F:metalloproteidase activity; TAS.

DR GO; GO:0007283; P:spermatogenesis; TAS.

DR InterPro; IPR006586; ADAM cysteine.

DR InterPro; IPR001762; Disintegrin.

DR InterPro; IPR006209; EGF like.

DR InterPro; IPR00625; Peptidase\_M12B.

DR InterPro; IPR001590; Peptidase\_M12B.

DR InterPro; IPR002870; Peptidase\_M12B\_N.

DR Pfam; PR00200; disintegrin; 1.

DR Pfam; PR01562; Pep\_M12B\_propep; 1.

DR PRINTS; PR00289; DISINTEGRIN.

DR PRODOM; PD000664; Disintegrin; 1.

DR SMART; SM000608; ACR; 1.

DR SMART; SM00050; DISIN; 1.

DR PROSITE; PS50215; ADAM\_MEPRO; 1.

DR PROSITE; PS00427; DISINTEGRIN\_1; FALSE\_NEG.

DR PROSITE; PS50214; DISINTEGRIN\_2; 1.

DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.

DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.

DR PROSITE; PS00142; ZINC\_PROTEASE; FALSE NEG.

KW Signal; Glycoprotein; Transmembrane; EGF-like domain;

KW Alternative splicing; Repeat.

FT SIGNAL 1 18 POTENTIAL.

FT PROPEP 19 193 BY SIMILARITY.

FT CHAIN 194 820 ADAM\_29.

FT DOMAIN 194 674 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 675 695 POTENTIAL.

FT DOMAIN 194 390 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 397 483 METALLOPROTEASE-LIKE.

FT DOMAIN 484 624 DISINTEGRIN-LIKE.

FT DOMAIN 625 654 CYS-RICH.

FT DOMAIN 669 675 EGF-LIKE.

FT DOMAIN 739 819 POLY-LYS.

FT REPEAT 739 747 9 X 9 AA APPROXIMATE REPEATS.

FT REPEAT 748 756 1.

FT REPEAT 757 765 2.

FT REPEAT 766 774 3.

FT REPEAT 775 783 4.

FT REPEAT 784 792 5.

FT REPEAT 793 801 6.

FT REPEAT 802 810 7.

FT REPEAT 811 819 8.

FT DISULFID 307 384 9.

FT DISULFID 347 369 BY SIMILARITY.

FT DISULFID 455 468 BY SIMILARITY.

FT DISULFID 625 636 BY SIMILARITY.

FT DISULFID 630 642 BY SIMILARITY.

FT DISULFID 644 653 BY SIMILARITY.

FT CARBOHYD 217 217 N-LINKED (GLCNAC . .) (POTENTIAL).

FT CARBOHYD 320 320 N-LINKED (GLCNAC . .) (POTENTIAL).

FT CARBOHYD 368 368 N-LINKED (GLCNAC . .) (POTENTIAL).

FT CARBOHYD 428 428 N-LINKED (GLCNAC . .) (POTENTIAL).

FT CARBOHYD 469 469 N-LINKED (GLCNAC . .) (POTENTIAL).

FT CARBOHYD 538 538 N-LINKED (GLCNAC . .) (POTENTIAL).

FT CARBOHYD 545 545 N-LINKED (GLCNAC . .) (POTENTIAL).

FT CARBOHYD 558 558 N-LINKED (GLCNAC . .) (POTENTIAL).

FT CARBOHYD 564 564 N-LINKED (GLCNAC . .) (POTENTIAL).

FT VARSPLIC 750 803 Missing (in isoform Beta).

FT VARSPLIC 763 787 /FTId-VSP 005491. VMPSSOHPQLTPSQVPPVMSQSH -> QNLFLFSFSISD CYLNFRLLYQAT (in isoform Gamma).

FT VARSPLIC 788 820 /FTId=VSP 005492. Missing (in isoform Gamma).

FT VARSPLIC 196 196 /FTId=VSP 005493. H -> Y (IN REF. 2).

FT CONFLICT 744 P -> H (IN REF. 2).

FT CONFLICT 748 S -> Y (IN REF. 2).

FT CONFLICT 753 Q -> R (IN REF. 1; AAF03777).

FT CONFLICT 764 M -> T (IN REF. 2).

FT CONFLICT 769 773 HPQLT -> QPRVM (IN REF. 2).

SQ SEQUENCE 820 AA; 92753 MW; 1F54E9F8128E4C27 CRC64;

Query Match 100.0%; Score 615; DB 1; Length 820;

Best Local Similarity 100.0%; Pred. No. 1e-48; Mismatches 0; Indels 0; Gaps 0;

Matches 103; Conservative 0;

Qy 1 VHTKDIIFNVKRCGNGVVEEGECDCGPLKHCAKDPCCLSNCTLTDGSTCAFGLCCRDCKF 60

Db 389 VHTKDIIFNVKRCGNGVVEEGECDCGPLKHCAKDPCCLSNCTLTDGSTCAFGLCCRDCKF 448

Qy 61 LPSGKVCRKEVNECDLPEWCNGTSHKCPDDFYVEDGIPCKERG 103

Db 449 LPSGKVCRKEVNECDLPEWCNGTSHKCPDDFYVEDGIPCKERG 491

RESULT 2

AD20\_HUMAN STANDARD; PRT; 726 AA.

ID AD20\_HUMAN STANDARD; PRT; 726 AA.

AC O43506; Q9UKJ9;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE ADAM\_20 precursor (EC 3.4.24.-) (A disintegrin and metalloprotease domain 20).

GN ADAM20.

OS Homo sapiens (Human).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI\_TaxID=9606;

RN [1] RSEQUENCE FROM N.A.

RC TISSUE=Testis;

RX MEDLINE=98137801; PubMed=9469942;

RA Hooft van Huijsduijnen R.; "ADAM\_20 and 21; two novel human testis-specific membrane metalloproteases with similarity to fertilin-alpha." Gene 206:273-282 (1998).

RN [2] RSEQUENCE FROM N.A.

RX MEDLINE=99453762; PubMed=10524237;

RA Poindexter K., Nelson N., DuBose R.F., Black R.A., Cerretti D.P.; RT "The identification of seven metalloprotease-disintegrin (ADAM) genes from genomic libraries." Gene 237:61-70 (1999).

RL

CC -1- FUNCTION: May be involved in sperm maturation and/or fertilization.

CC -1- COFACTOR: Binds 1 zinc ion per subunit (Potential).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- TISSUE SPECIFICITY: Testis specific.

CC -1- DOMAIN: A tripeptide motif (VGE) within disintegrin-like domain could be involved in the binding to egg integrin receptor and thus could mediate sperm/egg binding.

CC -1- DOMAIN: The cysteine-rich domain encodes putative cell-fusion peptides, which could be involved in sperm-egg fusion.

CC -1- PTM: Has no obvious cleavage site for furin endopeptidase, suggesting that the proteolytic processing is regulated.

CC -1- MISCELLANEOUS: May be the functional equivalent of ADAM\_1/fertilin alpha which is a pseudogene in human.

CC -1- SIMILARITY: Belongs to peptidase family M12B.

CC -1- SIMILARITY: Contains 1 EGF-like domain.

CC -1- SIMILARITY: Contains 1 disintegrin domain.

CC

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COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/836,443  
 FILING DATE: 01-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 9709420  
 FILING DATE: 05-SEP-1997  
 APPLICATION NUMBER: 9526230.9  
 FILING DATE: 21-DEC-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Resnick, David S  
 REGISTRATION NUMBER: 34,235  
 REFERENCE/DOCKET NUMBER: 47424  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-523-3400  
 TELEFAX: 617-523-6440  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 751 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: Single  
 TOPOLOGY: linear  
 MOLECULE TYPE: No. 5883241e  
 US-08-836-443-3

Query Match 50.2%; Score 309; DB 2; Length 751;  
 Best Local Similarity 51.5%; Pred. No. 3.9e-20;  
 Matches 51; Conservative 16; Mismatches 30; Indels 2; Gaps 2;

Qy 3 TKDIFNVRKCGNGVVEEGEECDCGPLKHCAXDPC-LSNCTLTDGSTCAFGLCCDKCKFL 61  
 Db 235 TRMLYGGRRCGNGYLEDGEEDCGEEEEEBC-NNPCCNASNCTLRPGAECAHGSCHOCKLL 293

Query Match 47.0%; Score 289; DB 4; Length 787;  
 Best Local Similarity 55.1%; Pred. No. 2.5e-18;  
 Matches 49; Conservative 12; Mismatches 26; Indels 2; Gaps 2;

Qy 12 CGNGVVEEGEECDCGPLKHCAXDPCCLS-NCTLTGSTCAFGLCCDKCKFLPSGKVCRKE 70  
 Db 420 CGNGFVEAGEECDCGPQEC-RDLCCFAHNCSLRPGAAQCAHGDCCVRCILKPGALCRQA 478

RESULT 4  
 US-09-548-797B-5  
 ; Sequence 5, Application US/09548797B  
 ; Patent No. 6683165  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KEITH, TIM  
 ; TITLE OF INVENTION: NOVEL HUMAN GENE RELATING TO RESPIRATORY DISEASES AND  
 ; TITLE OF INVENTION: OBESITY  
 ; FILE REFERENCE: 2976-4039  
 ; CURRENT APPLICATION NUMBER: US/09/548,797B  
 ; CURRENT FILING DATE: 2002-11-26  
 ; PRIOR APPLICATION NUMBER: 60/129,391  
 ; PRIOR FILING DATE: 1999-04-13  
 ; NUMBER OF SEQ ID NOS: 170  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 787  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-548-797B-5

Query Match 47.0%; Score 289; DB 4; Length 787;  
 Best Local Similarity 55.1%; Pred. No. 2.5e-18;  
 Matches 49; Conservative 12; Mismatches 26; Indels 2; Gaps 2;

Qy 71 VNECDLPEWCGNTSHKCPDDFYVVEDGIPC 99  
 Db 479 MGDCDLPEFCTGTSSHCPDPVYLLDGSPC 507

RESULT 5  
 US-09-632-098-2  
 ; Sequence 2, Application US/09632098  
 ; Patent No. 6420154  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Bishop, Paul D.  
 ; APPLICANT: Baird, Nand  
 ; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES  
 ; FILE REFERENCE: 99-39  
 ; CURRENT APPLICATION NUMBER: US/09/632,098  
 ; CURRENT FILING DATE: 2000-08-02  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 802  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-632-098-2

Query Match 47.0%; Score 289; DB 4; Length 802;  
 Best Local Similarity 55.1%; Pred. No. 2.5e-18;  
 Matches 49; Conservative 12; Mismatches 26; Indels 2; Gaps 2;

Qy 12 CGNGVVEEGEECDCGPLKHCAXDPCCLS-NCTLTGSTCAFGLCCDKCKFLPSGKVCRKE 70  
 Db 420 CGNGFVEAGEECDCGPQEC-RDLCCFAHNCSLRPGAAQCAHGDCCVRCILKPGALCRQA 478

RESULT 3  
 US-09-548-797B-4  
 ; Sequence 4, Application US/09548797B  
 ; Patent No. 6683165  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KEITH, TIM  
 ; TITLE OF INVENTION: NOVEL HUMAN GENE RELATING TO RESPIRATORY DISEASES AND  
 ; TITLE OF INVENTION: OBESITY  
 ; FILE REFERENCE: 2976-4039  
 ; CURRENT APPLICATION NUMBER: US/09/548,797B  
 ; CURRENT FILING DATE: 2002-11-26  
 ; PRIOR APPLICATION NUMBER: 60/129,391  
 ; PRIOR FILING DATE: 1999-04-13  
 ; NUMBER OF SEQ ID NOS: 170  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 746  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-548-797B-4

Query Match 47.0%; Score 289; DB 4; Length 746;  
 Best Local Similarity 55.1%; Pred. No. 2.4e-18;  
 Matches 49; Conservative 12; Mismatches 26; Indels 2; Gaps 2;

Qy 12 CGNGVVEEGEECDCGPLKHCAXDPCCLS-NCTLTGSTCAFGLCCDKCKFLPSGKVCRKE 70  
 Db 479 MGDCDLPEFCTGTSSHCPDPVYLLDGSPC 507



